

CONSTELLATION MAPPING AND USES THEREOF

ABSTRACT OF THE DISCLOSURE

The present invention features computer methods and systems for comparing biomolecules across biological samples. In these methods, mass spectrometry measurements are obtained on biomolecules in two or more samples. These measurements are then processed and analyzed by the methods described herein to render them more comparable. We refer to this technology as “Constellation Mapping” (CM). The resulting data, constellation maps, can be used to compare the abundance of biomolecules across samples, and, when done in real time, can be used to select differentially abundant biomolecules for subsequent LC/MS-MS.